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Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Mon Jun 04 19:49:29 EDT 2007

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Application No: 10581551 Version No: 1.1

**Input Set:****Output Set:**

**Started:** 2007-06-04 19:49:18.416  
**Finished:** 2007-06-04 19:49:22.284  
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 868 ms  
**Total Warnings:** 26  
**Total Errors:** 1  
**No. of SeqIDs Defined:** 84  
**Actual SeqID Count:** 84

Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (59)
W 213	Artificial or Unknown found in <213> in SEQ ID (60)
W 213	Artificial or Unknown found in <213> in SEQ ID (61)
W 213	Artificial or Unknown found in <213> in SEQ ID (62)
W 213	Artificial or Unknown found in <213> in SEQ ID (63)
W 213	Artificial or Unknown found in <213> in SEQ ID (64)
W 213	Artificial or Unknown found in <213> in SEQ ID (65)
W 213	Artificial or Unknown found in <213> in SEQ ID (66)
W 213	Artificial or Unknown found in <213> in SEQ ID (67)
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W 213	Artificial or Unknown found in <213> in SEQ ID (71)
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W 213	Artificial or Unknown found in <213> in SEQ ID (75)
W 213	Artificial or Unknown found in <213> in SEQ ID (76)
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**Input Set:**

**Output Set:**

**Started:** 2007-06-04 19:49:18.416  
**Finished:** 2007-06-04 19:49:22.284  
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 868 ms  
**Total Warnings:** 26  
**Total Errors:** 1  
**No. of SeqIDs Defined:** 84  
**Actual SeqID Count:** 84

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (78) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> MIYAWAKI, ATSUSHI  
KOGURE, TAKAKO  
HAMA, HIROSHI  
KINJO, MASATAKA  
SAITO, KENTA  
KARASAWA, SATOSHI  
ARAKI, TOSHIO

<120> FLUORESCENT PROTEIN

<130> P30056

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<141> 2007-05-25

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Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val  
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Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe  
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Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser  
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Cys	Tyr	Gly	His	Arg	Pro	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp	
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aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt	384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe	
115 120 125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca	432
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro	
130 135 140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt	480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val	
145 150 155 160	
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Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu  
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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe  
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Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro  
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Thr Leu Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Met  
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Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser  
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aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144  
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Cys Tyr Gly His Arg Cys Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp  
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 gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt	336
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 aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt	384
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Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro	
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Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Asp	
145 150 155 160	
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Thr Leu Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Met	
165 170 175	
 aag act act tac aag gcg gca aaa aag att ctt aaa atg cca gga agc	576
Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser	
180 185 190	
 cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act	624
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr	
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 Gly Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp	



65

70

75

80

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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

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Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro

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Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Asp

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Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Met

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Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe		
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Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro		
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Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Lys	Ile	Leu	Lys	Met	Pro	Gly	Ser		
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His	Tyr	Ile	Ser	His	Arg	Leu	Val	Arg	Lys	Thr	Glu	Gly	Asn	Ile	Thr		
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gag	ctg	gta	gaa	gat	gca	gta	gct	cat	tcc	taa						657	
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Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala		
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Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu  
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Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu  
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Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe  
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Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu	
85 90 95	
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt	336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu	
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aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt	384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe	
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Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro	
130 135 140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt	480
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val	
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